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► **To cite this version:**

Bernard Caromel, Jacques Lagnel, Carole Iampietro, Marie-Claire Le Coant, Marine Sallaberry, et al..
A reference genome of *Solanum habrochaites*. XVII SOLANACEAE2022 International Conference on
the Plant Family of Solanaceae, Nov 2022, THESSALONIKI, Greece. hal-04136943

HAL Id: hal-04136943

<https://hal.inrae.fr/hal-04136943>

Submitted on 21 Jun 2023

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XVII SOLANACEAE2022 International Conference on the Plant Family of Solanaceae November 1-5, 2022, THESSALONIKI, GREECE

POSTER PRESENTATION

A reference genome of *Solanum habrochaites*

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Related species have been used in tomato breeding as sources of resistance to many diseases. Genetic maps based on progenies issued from interspecific crosses highlighted chromosomal rearrangements between the cultivated tomato (*Solanum lycopersicum*) and related species. Genome rearrangements limit therefore the use of the tomato reference genome sequence to study interesting loci in related species. High-quality genomes from tomato-related species are available for *S. pimpinellifolium* and *S. pennellii*. However, no high-quality genome is available to date for *S. habrochaites*, a species carrying resistance to several pests and pathogens. We thus constructed a reference genome of *S. habrochaites*, using a combination of PacBio Hifi sequencing and Hi-C technology for scaffolding. Following the PacBio Hifi sequencing, we assembled the genome with a total size of 1.03Gbp in 959 contigs, with N50 of 14 Mb, using Hifiasm software. Then, the contigs were scaffolded using Hi-C data to obtain chromosome-scale pseudo-molecules. Finally, the assembly was polished using Illumina short reads. We aim to use this novel reference genome of *S. habrochaites* to accurately identify resistance QTLs in regions rearranged between the genomes of *S. habrochaites* and of cultivated tomato.

Key words: *Solanum habrochaites*, long-read sequencing, PacBio

Acknowledgment: We would like to thank the GenoToul bioinformatics platform (<http://bioinfo.genotoul.fr/>) for access to computing facilities. This work formed part of the CASDAR “DG-PHYTOM” project, which was financially supported by the French Ministry of Agriculture.